

REMARKS

Applicants hereby submit that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. The amendments in the specification merely replace the paper copy of the Sequence Listing with an amended Sequence Listing containing the consensus sequence shown in Figure 1. Furthermore, the amendments insert sequence identifiers in the specification. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050.

Date: Aug. 1, 2001

Respectfully submitted,

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“Version With Markings to Show Changes Made”

In the specification:

Paragraph beginning at page 4, line 2, has been amended as follows:

Fig. 1, *Mycobacterium Tuberculosis*, rat HSP 60 and human HSP 60 (sequences P06806, P19227 and P10809, corresponding to SEQ ID NOs:6, 7 and 8 respectively), were compared with pileup program from GCG-Wisconsin Package v9.0. The conserved regions are indicated (consensus; SEQ ID NO:9). Bold, underlined residues represent the preferred peptides.

Paragraph beginning at page 4, line 13, has been amended as follows:

Fig. 5, the common motif within peptides 6 (amino acid residues 31 to 46 of SEQ ID NO:6), 7 (amino acid residues 37 to 52 of SEQ ID NO:6) and R5 (amino acid residues 61 to 80 of SEQ ID NO:7), V--E--WG-P (amino acid residues 18 to 22 of SEQ ID NO:9) is shown.

Paragraph beginning at page 12, line 9, has been amended as follows:

It is interesting to note that one of the two self protective epitopes is the self peptide 5, which is the homologous rat epitope to the bacterial protective peptide 6. Moreover, immunization with the bacterial peptides 6 and 7 and with the mammalian peptide 5 led to the production of anti bacterial HSP 6 and anti bacterial HSP antibodies, as well as protection against disease induction. Observing the primary structure of these three peptides leads to the conclusion that they express a common motif (V--E--W G-P; amino acid residues 18 to 22 of SEQ ID NO:9) which might be the protective motif of these peptides (Figure. 5).

Table 4 beginning at page 20, line 1, has been amended as follows:

Table 4
Potential epitopes of MT HSP 65kD

Location of the peptide (aa residues of SEQ ID NO:6)	Sequence of the peptide	Length	Experimental peptide matching
35-43	<u>G-RNVVLEKKW-G</u>	9	6,7
123-132	<u>A-VEKVTETLLK-G</u>	10	21
135-143	<u>A-KEVETKEQI-A</u>	9	21
319-332	RKVVVTKDAETTIVE	14	none
357-367	<u>S-DYDREKLQERL-A</u>	11	59
383-396	<u>A-TEVELKERKHRIED-A</u>	14	63
183-195	<u>G-LQLELTEGMRFDK-G</u>	13	31
259-270	<u>S-TLVVNKIRGTFK-S</u>	12	45

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